



SEQUENCE LISTING

<110> Puchta, Holger
Braun, Christian

<120> Recombination systems and methods for eliminating nucleic acid sequences from genome of eukaryotic organisms

<130> 53262-20031.00/13173-00010-US

<140> US 10/750,891

<141> 2004-01-05

<150> PCT/EP02/07281

<151> 2002-07-02

<150> DE 101 31 786.7

<151> 2001-07-04

<160> 30

<170> PatentIn version 3.3

<210> 1

<211> 788

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (62)..(766)

<223> open reading frame coding for I-SceI

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g atg aaa aac atc aaa aac cag gta atg aac ctg ggt ccg aac tct 109

Met Lys Asn Ile Lys Lys Asn Gln Val Met Asn Leu Gly Pro Asn Ser
1 5 10 15

aaa ctg ctg aaa gaa tac aaa tcc cag ctg atc gaa ctg aac atc gaa 157
Lys Leu Lys Glu Tyr Lys Ser Gln Leu Ile Glu Leu Asn Ile Glu
20 25 30

cag ttc gaa gca ggt atc ggt ctg atc ctg ggt gat gct tac atc cgt 205
Gln Phe Glu Ala Gly Ile Gly Leu Ile Leu Gly Asp Ala Tyr Ile Arg
35 40 45

tct cgt gat gaa ggt aaa acc tac tgt atg cag ttc gag tgg aaa aac 253
Ser Arg Asp Glu Gly Lys Thr Tyr Cys Met Gln Phe Glu Trp Lys Asn
50 55 60

aaa gca tac atg gac cac gta tgt ctg ctg tac gat cag tgg gta ctg 301
Lys Ala Tyr Met Asp His Val Cys Leu Leu Tyr Asp Gln Trp Val Leu
65 70 75 80

tcc ccg ccg cac aaa aaa gaa cgt gtt aac cac ctg ggt aac ctg gta 349
Ser Pro Pro His Lys Lys Glu Arg Val Asn His Leu Gly Asn Leu Val
85 90 95

atc acc tgg ggc gcc cag act ttc aaa cac caa gct ttc aac aaa ctg 397
Ile Thr Trp Gly Ala Gln Thr Phe Lys His Gln Ala Phe Asn Lys Leu
100 105 110

gct agc ctg ttc atc gtt aac aac aaa aaa acc atc ccg aac aac ctg 445
Ala Ser Leu Phe Ile Val Asn Asn Lys Lys Thr Ile Pro Asn Asn Leu
115 120 125

gtt gaa aac tac ctg acc ccg atg tct ctg gca tac tgg ttc atg gat		493
Val Glu Asn Tyr Leu Thr Pro Met Ser Leu Ala Tyr Trp Phe Met Asp		
130 135 140		
gat ggt aaa tgg gat tac aac aaa aac tct acc aac aaa tcg atc		541
Asp Gly Gly Lys Trp Asp Tyr Asn Lys Asn Ser Thr Asn Lys Ser Ile		
145 150 155 160		
gta ctg aac acc cag tct ttc act ttc gaa gaa gta gaa tac ctg gtt		589
Val Leu Asn Thr Gln Ser Phe Thr Phe Glu Glu Val Glu Tyr Leu Val		
165 170 175		
aag ggt ctg cgt aac aaa ttc caa ctg aac tgt tac cta aaa atc aac		637
Lys Gly Leu Arg Asn Lys Phe Gln Leu Asn Cys Tyr Leu Lys Ile Asn		
180 185 190		
aaa aac aaa ccg atc atc tac atc gat tct atg tct tac ctg atc ttc		685
Lys Asn Lys Pro Ile Ile Tyr Ile Asp Ser Met Ser Tyr Leu Ile Phe		
195 200 205		
tac aac ctg atc aaa ccg tac ctg atc ccg cag atg atg tac aaa ctg		733
Tyr Asn Leu Ile Lys Pro Tyr Leu Ile Pro Gln Met Met Tyr Lys Leu		
210 215 220		
ccg aac act atc tcc tcc gaa act ttc ctg aaa taataagtgc agtactggat		786
Pro Asn Thr Ile Ser Ser Glu Thr Phe Leu Lys		
225 230 235		
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<210> 2
<211> 235
<212> PRT
<213> *Saccharomyces cerevisiae*

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20 25 30		
Gln Phe Glu Ala Gly Ile Gly Leu Ile Leu Gly Asp Ala Tyr Ile Arg		
35 40 45		
Ser Arg Asp Glu Gly Lys Thr Tyr Cys Met Gln Phe Glu Trp Lys Asn		
50 55 60		
Lys Ala Tyr Met Asp His Val Cys Leu Leu Tyr Asp Gln Trp Val Leu		
65 70 75 80		
Ser Pro Pro His Lys Lys Glu Arg Val Asn His Leu Gly Asn Leu Val		
85 90 95		
Ile Thr Trp Gly Ala Gln Thr Phe Lys His Gln Ala Phe Asn Lys Leu		
100 105 110		
Ala Ser Leu Phe Ile Val Asn Asn Lys Lys Thr Ile Pro Asn Asn Leu		
115 120 125		
Val Glu Asn Tyr Leu Thr Pro Met Ser Leu Ala Tyr Trp Phe Met Asp		
130 135 140		
Asp Gly Gly Lys Trp Asp Tyr Asn Lys Asn Ser Thr Asn Lys Ser Ile		
145 150 155 160		
Val Leu Asn Thr Gln Ser Phe Thr Phe Glu Glu Val Glu Tyr Leu Val		
165 170 175		
Lys Gly Leu Arg Asn Lys Phe Gln Leu Asn Cys Tyr Leu Lys Ile Asn		
180 185 190		
Lys Asn Lys Pro Ile Ile Tyr Ile Asp Ser Met Ser Tyr Leu Ile Phe		
195 200 205		
Tyr Asn Leu Ile Lys Pro Tyr Leu Ile Pro Gln Met Met Tyr Lys Leu		
210 215 220		
Pro Asn Thr Ile Ser Ser Glu Thr Phe Leu Lys		
225 230 235		

Pro Phe Leu Val Asp Cys Met Arg Tyr Lys Val Ser Asp Gly Asn Lys
 210 215 220 225
 ggc cac ctt tagctcgag 746
 Gly His Leu

<210> 4
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<212> PRT
<213> Chlamydomonas appplanata

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Thr Gly Ser Val Gly Arg Thr Trp Arg Tyr Arg Ala Leu His Lys Ser
 35 40 45
Glu His Gln Thr Tyr Leu Phe His Lys Tyr Glu Ile Leu Lys Pro Leu
 50 55 60
Cys Gly Glu Asn Thr Leu Pro Thr Glu Ser Ile Val Phe Asp Glu Arg
 65 70 75 80
Thr Asn Lys Glu Val Lys Arg Trp Phe Phe Asn Thr Leu Thr Asn Pro
 85 90 95
Ser Leu Lys Phe Phe Ala Asp Met Phe Tyr Thr Tyr Asp Gln Asn Thr
 100 105 110
Gln Lys Trp Val Lys Asp Val Pro Val Lys Val Gln Thr Phe Leu Thr
 115 120 125
Pro Gln Ala Leu Ala Tyr Phe Tyr Ile Asp Asp Gly Ala Leu Lys Trp
 130 135 140
Leu Asn Lys Ser Asn Ala Met Gln Ile Cys Thr Glu Ser Phe Ser Gln
 145 150 155 160
Gly Gly Thr Ile Arg Ile Gln Lys Ala Leu Lys Thr Leu Tyr Asn Ile
 165 170 175
Asp Thr Thr Leu Thr Lys Lys Thr Leu Gln Asp Gly Arg Ile Gly Tyr
 180 185 190
Arg Ile Ala Ile Pro Glu Ala Ser Ser Gly Ala Phe Arg Glu Val Ile
 195 200 205
Lys Pro Phe Leu Val Asp Cys Met Arg Tyr Lys Val Ser Asp Gly Asn
 210 215 220
Lys Gly His Leu
 225

<210> 5
<211> 582
<212> DNA
<213> Chlamydomonas reinhardtii

<220>
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<222> (55)..(573)
<223> openreading frame coding for I-CreI with nuclear
location signal

<220>
<221> misc_feature
<222> (55)..(84)
<223> coding for nuclear location signal

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 Gly Pro Lys Lys Lys Arg Lys Val Ile Met Asn Thr Lys Tyr Asn Lys
 5 10 15
 gag ttc tta ctc tac tta gca ggg ttt gta gac ggt gac ggt agc ata 153
 Glu Phe Leu Leu Tyr Leu Ala Gly Phe Val Asp Gly Asp Gly Ser Ile
 20 25 30
 atc gct caa att aag cct aat cag tct tat aaa ttt aag cat cag cta 201
 Ile Ala Gln Ile Lys Pro Asn Gln Ser Tyr Lys Phe Lys His Gln Leu
 35 40 45
 tca ctc gcg ttc caa gtc acg caa aag aca cag aga cgt tgg ttt tta 249
 Ser Leu Ala Phe Gln Val Thr Gln Lys Thr Gln Arg Arg Trp Phe Leu
 50 55 60 65
 gac aaa tta gtg gat gaa att ggg gtt ggt tat gta aga gat agg ggt 297
 Asp Lys Leu Val Asp Glu Ile Gly Val Gly Tyr Val Arg Asp Arg Gly
 70 75 80
 agc gtt tcg gat tat att cta agc gaa atc aag cct ttg cat aat ttt 345
 Ser Val Ser Asp Tyr Ile Leu Ser Glu Ile Lys Pro Leu His Asn Phe
 85 90 95
 tta aca caa cta caa cct ttt cta aaa cta aaa caa aaa caa gca aat 393
 Leu Thr Gln Leu Gln Pro Phe Leu Lys Leu Lys Gln Lys Gln Ala Asn
 100 105 110
 tta gtt tta aaa att att gaa caa ctt ccg tca gca aaa gaa tcc ccg 441
 Leu Val Leu Lys Ile Ile Glu Gln Leu Pro Ser Ala Lys Glu Ser Pro
 115 120 125
 gac aaa ttc tta gaa gtt tgt aca tgg gtg gat caa att gca gct ctg 489
 Asp Lys Phe Leu Glu Val Cys Thr Trp Val Asp Gln Ile Ala Ala Leu
 130 135 140 145
 aat gat tcg aag acg cgt aaa aca act tct gaa acc gtt cgt gct gtg 537
 Asn Asp Ser Lys Thr Arg Lys Thr Ser Glu Thr Val Arg Ala Val
 150 155 160
 cta gac agt tta agt gaa aaa aag aaa tcg tcc ccg tagctcgag 582
 Leu Asp Ser Leu Ser Glu Lys Lys Lys Ser Ser Pro
 165 170

<210> 6
<211> 173
<212> PRT
<213> Chlamydomonas reinhardtii

<400> 6
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 20 25 30
 Ile Ile Ala Gln Ile Lys Pro Asn Gln Ser Tyr Lys Phe Lys His Gln
 35 40 45
 Leu Ser Leu Ala Phe Gln Val Thr Gln Lys Thr Gln Arg Arg Trp Phe
 50 55 60
 Leu Asp Lys Leu Val Asp Glu Ile Gly Val Gly Tyr Val Arg Asp Arg
 65 70 75 80
 Gly Ser Val Ser Asp Tyr Ile Leu Ser Glu Ile Lys Pro Leu His Asn
 85 90 95
 Phe Leu Thr Gln Leu Gln Pro Phe Leu Lys Leu Lys Gln Lys Gln Ala
 100 105 110
 Asn Leu Val Leu Lys Ile Ile Glu Gln Leu Pro Ser Ala Lys Glu Ser

115	120	125
Pro Asp Lys Phe Leu Glu Val Cys Thr Trp Val Asp Gln Ile Ala Ala		
130	135	140
Leu Asn Asp Ser Lys Thr Arg Lys Thr Thr Ser Glu Thr Val Arg Ala		
145	150	155
Val Leu Asp Ser Leu Ser Glu Lys Lys Lys Ser Ser Pro		
165	170	

<210> 7
<211> 546
<212> DNA
<213> Chlamydomonas segnis

<220>
<221> CDS
<222> (52)..(537)
<223> open readings frame coding for I-CpaI with nuclear
location signal

<220>
<221> misc_feature
<222> (52)..(81)
<223> coding for nuclear location signal

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Pro Lys Lys Lys Arg Lys Val Ile Met Asp Ile Asn Pro Gln Trp Ile
5 10 15
aca ggt ttc gta gat ggg gaa ggt tgt ttt agt gta agt att ctt aga 153
Thr Gly Phe Val Asp Gly Glu Gly Cys Phe Ser Val Ser Ile Leu Arg
20 25 30
aat aat tcg ttg cgc tat ggc cat cag ctt caa cca gaa ttc gta gtg 201
Asn Asn Ser Leu Arg Tyr Gly His Gln Leu Gln Pro Glu Phe Val Val
35 40 45 50
acc caa cat aaa tta gat gca aat gtt tta tat gca tta aaa gac tac 249
Thr Gln His Lys Leu Asp Ala Asn Val Leu Tyr Ala Leu Lys Asp Tyr
55 60 65
ttt aaa gtt gga tca gtc gtt gtg aat cat ggg gaa cgg ctt tgc tat 297
Phe Lys Val Gly Ser Val Val Asn His Gly Glu Arg Leu Cys Tyr
70 75 80
aaa gtc aaa aat att gat cac ttt ata acc gtc att ata cca ttt ttc 345
Lys Val Lys Asn Ile Asp His Phe Ile Thr Val Ile Ile Pro Phe Phe
85 90 95
gaa aaa cat gag cta aaa aca aaa aga aga att gaa ttt ctt cga ttt 393
Glu Lys His Glu Leu Lys Thr Lys Arg Arg Ile Glu Phe Leu Arg Phe
100 105 110
cga aaa atc tgc ttg ctg tta aaa gca ggt aga cat tta gaa tcg cag 441
Arg Lys Ile Cys Leu Leu Lys Ala Gly Arg His Leu Glu Ser Gln
115 120 125 130
gaa gga ttc gag aaa gtg ttg gat tta gca aaa aaa ctc cgt atc aat 489
Glu Gly Phe Glu Lys Val Leu Asp Leu Ala Lys Lys Leu Arg Ile Asn
135 140 145
gag aaa aac tac cag gaa tct atc aaa cgt ttt gaa gaa act ggc gag 537
Glu Lys Asn Tyr Gin Glu Ser Ile Lys Arg Phe Glu Glu Thr Gly Glu
150 155 160
taactcgag 546

<210> 8
<211> 162
<212> PRT
<213> Chlamydomonas segnis

<400> 8
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Trp Ile Thr Gly Phe Val Asp Gly Glu Gly Cys Phe Ser Val Ser Ile
20 25 30
Leu Arg Asn Asn Ser Leu Arg Tyr Gly His Gln Leu Gln Pro Glu Phe
35 40 45
Val Val Thr Gln His Lys Leu Asp Ala Asn Val Leu Tyr Ala Leu Lys
50 55 60
Asp Tyr Phe Lys Val Gly Ser Val Val Asn His Gly Glu Arg Leu
65 70 75 80
Cys Tyr Lys Val Lys Asn Ile Asp His Phe Ile Thr Val Ile Ile Pro
85 90 95
Phe Phe Glu Lys His Glu Leu Lys Thr Lys Arg Arg Ile Glu Phe Leu
100 105 110
Arg Phe Arg Lys Ile Cys Leu Leu Lys Ala Gly Arg His Leu Glu
115 120 125
Ser Gln Glu Gly Phe Glu Lys Val Leu Asp Leu Ala Lys Lys Leu Arg
130 135 140
Ile Asn Glu Lys Asn Tyr Gln Glu Ser Ile Lys Arg Phe Glu Glu Thr
145 150 155 160
Gly Glu

<210> 9
<211> 793
<212> DNA
<213> Chlamydomonas segnis

<220>
<221> CDS
<222> (53)..(784)
<223> open reading frame coding for I-CpaII with nuclear
location signal

<220>
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<222> (53)..(82)
<223> coding for nuclear location signal

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Pro Lys Lys Lys Arg Lys Val Ile Met Thr Asp Ser Lys Ser Arg Asn
5 10 15
aac aat aat ttt tta agc aat aat ctt tta cct ttg acc gat gac gag 154
Asn Asn Asn Phe Leu Ser Asn Asn Leu Leu Pro Leu Thr Asp Asp Glu
20 25 30
aag gct tta att gcg ggg aca ctt tta ggg gat gct cat att caa aag 202
Lys Ala Leu Ile Ala Gly Thr Leu Leu Gly Asp Ala His Ile Gln Lys
35 40 45 50

cgt ggt gat agc tat agg cta aaa ata gct cat ggc ttg gat cat gaa	250
Arg Gly Asp Ser Tyr Arg Leu Lys Ile Ala His Gly Leu Asp His Glu	
55 . 60 65	
gag ctt gtc gtc tgg aag tat aac cgt tta atc agg ttg tgt caa aca	298
Glu Leu Val Val Trp Lys Tyr Asn Arg Leu Ile Arg Leu Cys Gln Thr	
70 75 80	
aca caa ccc cca agg gtg gaa acc tac tca aca aag tta aag tct ggc	346
Thr Gln Pro Pro Arg Val Glu Thr Tyr Ser Thr Lys Leu Lys Ser Gly	
85 90 95	
gta ttg cct caa ggg gtt gtt ttc tat acc tcg tcc gga aag tat tta	394
Val Leu Pro Gln Gly Val Val Phe Tyr Thr Ser Ser Gly Lys Tyr Leu	
100 105 110	
aaa gag act tat gac ctt ttt tat aaa caa act gca gac ggt cggt agg	442
Lys Glu Thr Tyr Asp Leu Phe Tyr Lys Gln Thr Ala Asp Gly Arg Arg	
115 120 125 130	
gta aaa aca ata aca cag gag ttg atc gac agt tta ccc aag cat cca	490
Val Lys Thr Ile Thr Gln Glu Leu Ile Asp Ser Leu Pro Lys His Pro	
135 140 145	
ttg gtc tta gca gcc ttt ttt atg gac gat ggt agt gtt cgg tcc gac	538
Leu Val Leu Ala Ala Phe Phe Met Asp Asp Gly Ser Val Arg Ser Asp	
150 155 160	
tgt tat tca gga aag att gca acg cca ggg ttt gct ggt aaa gaa gaa	586
Cys Tyr Ser Gly Lys Ile Ala Thr Pro Gly Phe Ala Gly Lys Glu Glu	
165 170 175	
agc cag ttg ttg tgt aac tat cta cac agt tgg gat gtt caa gca aac	634
Ser Gln Leu Leu Cys Asn Tyr Leu His Ser Trp Asp Val Gln Ala Asn	
180 185 190	
gta gtt gct cat aaa aaa gca aac aat cag tat tac att ggg ctc cca	682
Val Val Ala His Lys Lys Ala Asn Asn Gln Tyr Tyr Ile Gly Leu Pro	
195 200 205 210	
gca aaa aca ttt ggt cgc ttt att aac att att gaa ccc tac gtt aga	730
Ala Lys Thr Phe Gly Arg Phe Ile Asn Ile Ile Glu Pro Tyr Val Arg	
215 220 225	
gaa gtt cct gct tta tgt tat aaa tta aac gaa tca aga aaa ccc cgt	778
Glu Val Pro Ala Leu Cys Tyr Lys Leu Asn Glu Ser Arg Lys Pro Arg	
230 235 240	
aac gac tgactcgag	793
Asn Asp	

<210> 10
<211> 244
<212> PRT
<213> Chlamydomonas segnis

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      20          25          30
Asp Glu Lys Ala Leu Ile Ala Gly Thr Leu Leu Gly Asp Ala His Ile
      35          40          45
Gln Lys Arg Gly Asp Ser Tyr Arg Leu Lys Ile Ala His Gly Leu Asp
      50          55          60
His Glu Glu Leu Val Val Trp Lys Tyr Asn Arg Leu Ile Arg Leu Cys
      65          70          75          80
Gln Thr Thr Gln Pro Pro Arg Val Glu Thr Tyr Ser Thr Lys Leu Lys
      85          90          95
Ser Gly Val Leu Pro Gln Gly Val Val Phe Tyr Thr Ser Ser Gly Lys
      100         105         110

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Tyr Leu Lys Glu Thr Tyr Asp Leu Phe Tyr Lys Gln Thr Ala Asp Gly
    115          120          125
Arg Arg Val Lys Thr Ile Thr Gln Glu Leu Ile Asp Ser Leu Pro Lys
    130          135          140
His Pro Leu Val Leu Ala Ala Phe Phe Met Asp Asp Gly Ser Val Arg
    145          150          155          160
Ser Asp Cys Tyr Ser Gly Lys Ile Ala Thr Pro Gly Phe Ala Gly Lys
    165          170          175
Glu Glu Ser Gln Leu Leu Cys Asn Tyr Leu His Ser Trp Asp Val Gln
    180          185          190
Ala Asn Val Val Ala His Lys Lys Ala Asn Asn Gln Tyr Tyr Ile Gly
    195          200          205
Leu Pro Ala Lys Thr Phe Gly Arg Phe Ile Asn Ile Ile Glu Pro Tyr
    210          215          220
Val Arg Glu Val Pro Ala Leu Cys Tyr Lys Leu Asn Glu Ser Arg Lys
    225          230          235          240
Pro Arg Asn Asp

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<210> 11
<211> 35
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of the artificial sequence:
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<400> 11
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<210> 12
<211> 120
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of the artificial sequence:
 oligonucleotide primer

<400> 12
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ggtccaaaga aaaagagaaaa ggttatcatg aatacaaaaat ataataaaaga gttcttactc 120

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<210> 13  
<211> 116  
<212> DNA  
<213> Artificial Sequence
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<220>
<223> Description of the artificial sequence:
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ggtccaaaga aaaagagaaaa ggttatcatg gacattaatc ctcaatggat tacagg 116
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<210> 14
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide primer

<400> 14
cggttcgagt tactcgccag tttcttcaaa acg 33

<210> 15
<211> 114
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide primer

<400> 15
cggttcgagt acctagaata caaagaagag gaagaagaaa cctctacaga agaagccatg 60
ggtccaaaga aaaagagaaa ggttatcatg accgattcta aatctagaaa caac 114

<210> 16
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide primer

<400> 16
cggttcgagc taaagggtggc ctttattgcc atcag 35

<210> 17
<211> 114
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide primer

<400> 17
cggttcgagt acctagaata caaagaagag gaagaagaaa cctctacaga agaagccatg 60
ggtccaaaga aaaagagaaa ggttatcatg tcattaacac aacaacaaaa agac 114

<210> 18
<211> 35
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 18
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<210> 19
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide primer

<400> 19
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taacag 66

<210> 20
<211> 65
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide primer

<400> 20
cggtctaga ctattaccct gttatcccta ggcccgatct agtaacatag atgacaccgc 60
gcgcg 65

<210> 21
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide primer

<400> 21
cggaagcttc gtcaccaatc ccaattcgat ctac 34

<210> 22
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide primer

<400> 22
cggaagcttc cacttgaaaa gtcccgctag tgcc 34

<210> 23
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide primer

<400> 23
cggaagcttc gtcaccaatc ccaattcgat ctac 34

<210> 24
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide primer

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<210> 25
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide primer

<400> 25
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tc 62

<210> 26
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:
oligonucleotide primer

<400> 26
ctaggatgag ccgtcatcga ggtgccaaac cttcagatta aaatgtctca cgacgtttg 60
ta 62

<210> 27
<211> 75
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 27

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gtaactctgt gccag 75

<210> 28

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 28

ctagctggca cagagttacc gggtaattt cgctaccta ggatcgtaac caatatgtct 60
cacggcggtt tcgga 75

<210> 29

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence: nuclear
location sequence

<400> 29

Pro Lys Thr Lys Arg Lys Val
1 5

<210> 30

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence: nuclear
location sequence

<400> 30

Pro Lys Lys Lys Arg Lys Val
1 5